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[illegible]

55 TCATCAGCGTTTGGCGTGGCTGTCGTGCGTTCGCCCTCCCTTCTGAGCGCCGGCTTTCGCGCGCGCCGCTTCGCCACTCGCGCTCTCCCTCCTCTGTCGGCGCCCTTTTCTCGCGCTTTCACCTTCTCTTCACTCCT

213 CCCTGCCCCCAAGACCCGCGCGCCCGGACGAGCTCTGGGGAGACGACGAGAAAGTATAGCTTCTACCATTTGAGCTCAATGCCTGTGTGAACTGGAAAGAAAACCA ATG TAT AAG CCC GTG GAC CCT CAC TCT CGG ATG CAG
met tyr lys pro val asp pro his ser arg met gln

ser thr ser ser tyr gly met arg gly gly ala tyr pro pro arg tyr phe tyr pro phe pro val pro leu leu ser val gly gly gln gln phe asn gly
361 TCC ACC TAC AGC TAT GGC ATG CGT GGA GGT GCC TAT CCC CCC AGA TAC TTT TAC CCA TTT CCA GTC CCA CCT TTA CTC TAC CAA GTT GAG CTC TCC GTG GGC GGA CAG CAG TTT AAT GGG

lys gly lys met arg pro pro val lys his asp ala pro ala arg ala leu arg thr leu gln ser glu pro glu arg leu glu val asn gly arg glu ala glu glu asn
81 AAA GGA AAG ATG AGA CCA CCC GTG AAA CAC GAT GCC CCT GCC CCT GGC ACT GGC CAG ACT GAA CCC CTG CCA GAA ACC TTC CAG CTA AAC CAC CAA AAC

[illegible]

ser val gly glu phe val gly glu gly lys ser lys lys ile ser lys lys asn ala ala arg ala val leu glu gln leu arg arg leu pro ala val glu arg

val lys pro arg ile lys lys ser gln pro thr cys lys thr ala pro asp tyr gln gly met asn pro ile ser arg leu ala gln ile gln ala lys lys gln lys glu

pro glu tyr met leu thr glu arg gly leu pro arg arg glu phe val met gln val lys val gly his thr ala glu gly val gly thr asn lys lys val ala lys arg

asn ala ala glu aan met leu glu ile leu gly phe lys val pro gln ala gln pro ala lys pro ala leu lys ser glu glu lys thr pro val lys lys pro gly asp gly arg lys

val thr phe phe glu pro ser pro gly asp glu asn gly thr ser asn lys asp glu phe arg met pro tyr leu ser his dln qln leu pro ala qly ile leu pro met val pro

[illegible]

nly thr ser pro thr ala glu thr tle lau lvs ser een tle ser ser glv kile wal pro kile glv eca arg thr arg eca ser glv ala leu tuc tuc eu cot ser eca ala ala abt sta
 3321 gaa gti gcc cag gct gtc ggg gtt agt caa gga cac cac acc aaa gat ttc acc agg gca gct cca aat cct gcc aag gca acg gta act gcc atg ata gcc cga gag ttg ttg tac ggg

441 GGC ACC TCG CCC ACA GCC GAG ACC ATT TTA AAG AGT AAC ATC TCT TCA GGC CAC GTA CCC CAT GGA CCT CGC ACT AGA CCC TCT GAG CAA CTG TAC TAC CTT TCC AGA GCC CAG GGA TTC

561 CAG GTT GAA TAC AAC AAC AAG AAC GAG TGT GTA TCT CTC ATC AAC TGC TCC TCA CAG CCG CCT CTC AGT CAT GGC ATC GGC AAG GAT GTG GAG TCC TGT CAT

6861 GAT ATG GCT GCA CTG AAC ATT TTA AAG CTG CTG TCT GAG TTG GAC CAA CAG AGC ACA GAG ATG CCA AGA ACA GGA AAT GGA CCA GTT TCA GGG TGC GGG AGG TGC TGA ACCTTTTCTGGCCAC

9863 TGATGATGCTGTGCTCTTGCCATTCATCCAGACACAAACAGCCCCAGCGCTTCAGTTCCTGTTTTGCATCGTGACAAAGAGAGAGCAGCCAAATCTCTCATGCTGGCTCTTCGATGACTCTTGAAAAACCCGGAGACGCCACACAGAGAGGCCCTTA TAGC
12.12 GCCCCGGAGCTAAGCGACGAGAGAAA GSCCAGTGGTTCCTACTGCACATGACTGACTCAGCTCGGCCACACGTAGCACCACTGTACCACCTGCTTCTTCAGTTCATTTTTTTCCTTTGATTTGATACACACTATATATTTTTCATTTTCAGTTC

440 CAGCTTAGGACCTTTAAACCTTAGCTCAAAAGATATGGTCCCTTTTAACTTTATTTTAAAGGACAGACCTTTAAATATGACCCCTTACCCCAATTAACAGAAATTTGTCAAAAGAGGTGTTTCTTTAGGAGGTAGCTTTTTTTACCACACATACA
59 GGACATTTACCTTAGTGGCCAGAAAGACTACAGGCTGTGTCCCTAGAGGGCCCAATACAGTCAATTCACCTCTTAGTCCGGGAAAGGTGACAGGTTTCTTGGTGTGTTGTCACACAGGGGCAAGCAGATCAGCTGGCTGGCCCTGGGGGAAGAGCAATTTGTGGCT

FIGURE 1C

Comparison of human (HUM) and mouse (MUS) staufen sequences

[illegible]

FIGURE 1D

698 >RBD4 RBD4<
DRO ppkdklmdadnpitkllqlqqrkekepeifeliakngnetarrrofmeveasgstargtgnskklakrnaaqalfelleavvtvptnetqseecctsatmsavtapaveataegk
HUM -----GGINPIRLAQIOAAKEKEPEYTLTERGLP--RRREFVMQVKGNGHTAGTGTNKKVAKRNAENMLEILGFKVPQRPQPTKPAKSEKTPINKPGDGRKVTFFDPCGS
CEL -----ghqinpvvarliqvtqakskehptfelvaehgvs--kykefiliqvkygddvqogkgnkrlakraaeamlesigfvkplpppgtelkkkmdcdpslpeishwtgppptav
C PI V E K P F V GP H K F F V VG G G SKK AK AA AL L

818
DRO vpmvatpvgmpgillirnmktpakkrdqivivksnveskeeeankevavaaeenannsnagdsesgdsqateaaesalntetgentsgvseasnvgantdgnnhaesknntes
HUM GDENGTSNKGEFRMP-----YLSHQQLPAGILPMVPEVAQAVGVSQCHHTDFTRAAPNP-AKATVTAMIARELLYGGTSP--TAETILKNN-----ISSGHVPHGPLTRPS---
CEL svsteepdtseaaqlspeqtdisekrelepdtekrvrtfnsgvhacpppgdqypnsivqelktdalvegkirkirrekenrraltaeqiveaeraqylqtktnttiqesqssah---

938 >RBD5 RBD5<
DRO ssenstansagvhmkeqllyleklldfevnfedypkgnhneflitvltsthpqi chgvkseeesqndaaenalkileklglnnamt*
HUM -----EQLDYLRSRVQGFQVEYKDFPNKNNKNEFVSLINCSQPPLISHGIGKOVESCHDMAALNLIKLLSELDOQOSTEMPPRTGNGPMVMVCGRC*
CEL -----hhleqlsdffkfelqytsfpqvgidqhtfivsigleaplvghgtgctteadenaaalalakkelseakt*
C G G SKK AK AA AL L

B)

230
STAUFEN GFKVTPORQPTKPAKSEKTPINKPGDGRKVTFFDPCSGDENGTSNKKEDEFRLPYLSHQQLPAGILPMVPEVAQAVGVSQCHHTKDFTRAAPNPAKATVTA
MAP1B KEKTKTKGPGTKTKSSSPVKSGDGKSKPLAASPAPAGLKESSDKVSRVSPKQKEEVEKAAPKPTTTPVKAARGEKDKKE TKNAANASASAKSATA
2247 2337

FIGURE 1' (cont'd)

A)

1

DRO mqhnhvaarpaphiraahhshahmhphgmeqhlgsalqqqqpppppppppphrdharlnhhhlhaqqqqqqqqtsenqaaavaaahghninenegeniensnqmqkirkqh
CEL
C. 2/15/05
(0.6 m A. 1.0 m)

121

DRO qhlaesnglignppppqafnplagnpaalaynqlpphphmaahlgsyaasppphymaqaakpakynhygenanengenennenyapkaillqntyrenqkvvvppvqvvtvpopp
CEL
m qavfet

241

DRO vttnnattstviasepvtqedsqkpetrqepasaddhvstgnidatgalenedtesgrgkdktpndlvnelarynki chqyzi teergpahckttvtlmlgd-eeysadgf
CEL
>RBD1
tltqmdgvmivqettdladlienaseaekseqlpohlphqwgqhkfeadptnfydytnakekekeamovaeiafnktrhvynlqdesgpahkkllftvklvltseetfegsgt

360

DRO kikaqhlasekaieetmykpppkirreogpparthitptvelnalamlqgtrfylldptqipptdsivppefagghlltappgmpqppppayalrqrlngfvpipsqpnphph
CEL
RBD1<
HUM
MCGGKGMKPFVDPFYSRQSTNYN-----

479

DRO ffnhggqrfppkfpafalppplgahvhgpnqfpevtppskittlvqkqfvgigrtlqqakhdaaalqvlk---tqalaaseeale-damdegdkkapiqvhelgikrnmv
CEL
>RBD2
>RBD3
HUM
MRGCAYPFRYFYPPF-VPLLYQVELSVGGQFNKGKTRQAAKHDAALRILO---NEPLPERLEVNGRESEENLNKSEISQVTE LALKRNLFP
CEL
lyappftlpidparpqgkqlqaviwningsiatgigtptlakdaaalavlepllrhngsdngfgenipvhkqkvisadihekaayqlkvnv
C. 2/15/05
G G SKK AK AA AL L
PI V E K
L R

595

DRO hfkvlreeppahmknfita---civgsiv---tegegngkvskkrraekmlvelqklppltpktqtplkrlkv-----ktpqksaaaregavvsgtdgtmqtkperrkrln
CEL
RBD3<
HUM
NTEVARESGPPHMQNFVK---VSVGEFV---GE GSKK18KONAAIAVLELKLQPLP-PAVERVKPRNK-
CEL
vfevlkeegpphdrqvvrcafvtegnvvkaeavqgkklkaeqaeactqllatvehltpennpvalatnvcktkklaamnrpkrtktivdkkmdply-----
C
F V GP H K F F V VG G G SKK AK AA AL L
Y L R M

FIGURE 1'

c)

FIGURE 1' (cont'd)

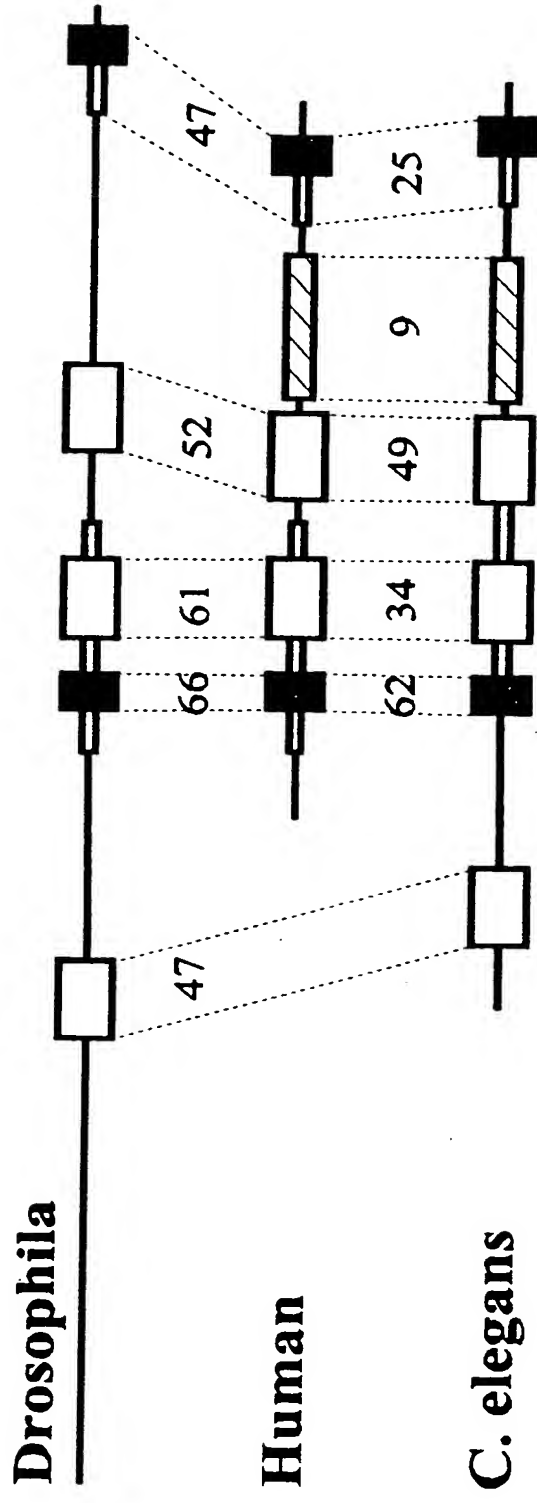
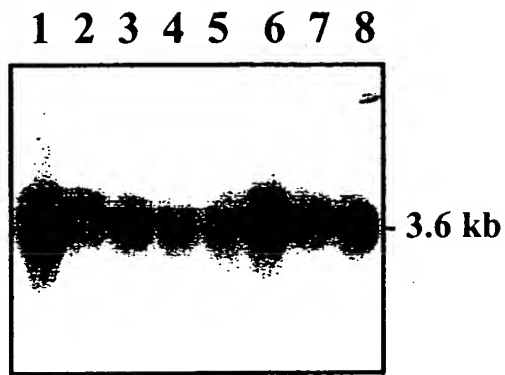
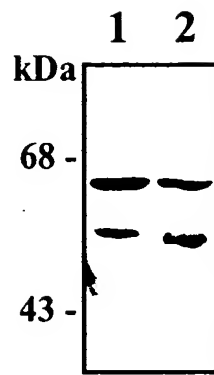


FIGURE 2

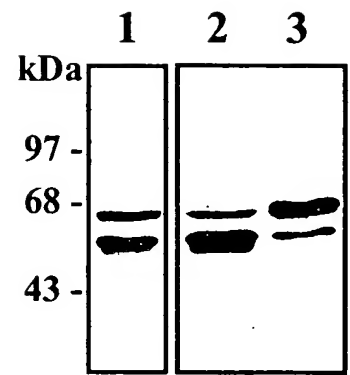
A



B



C



D

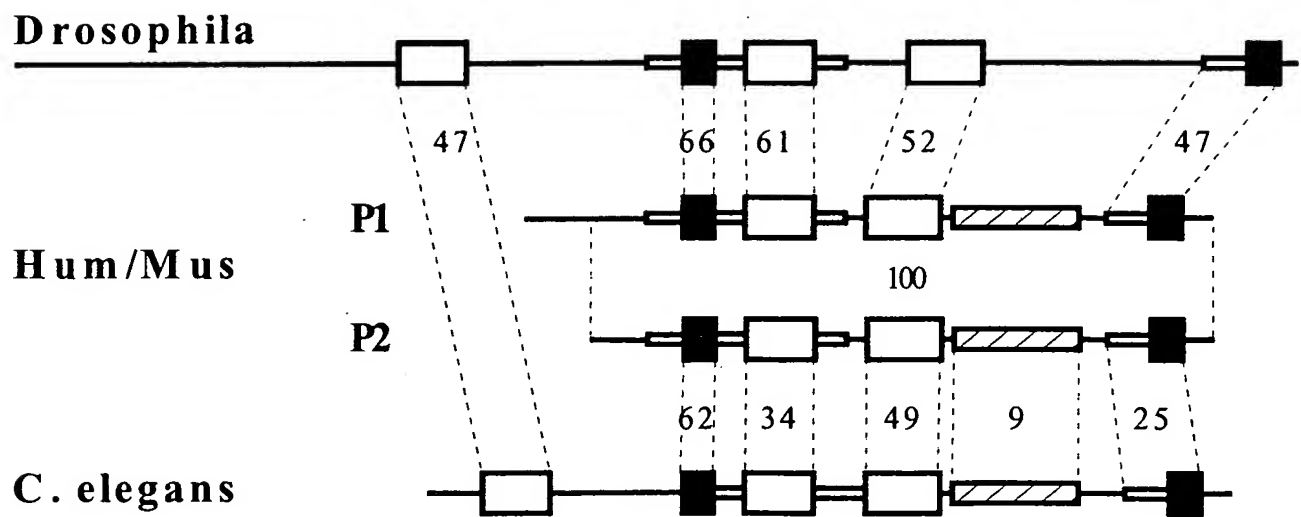
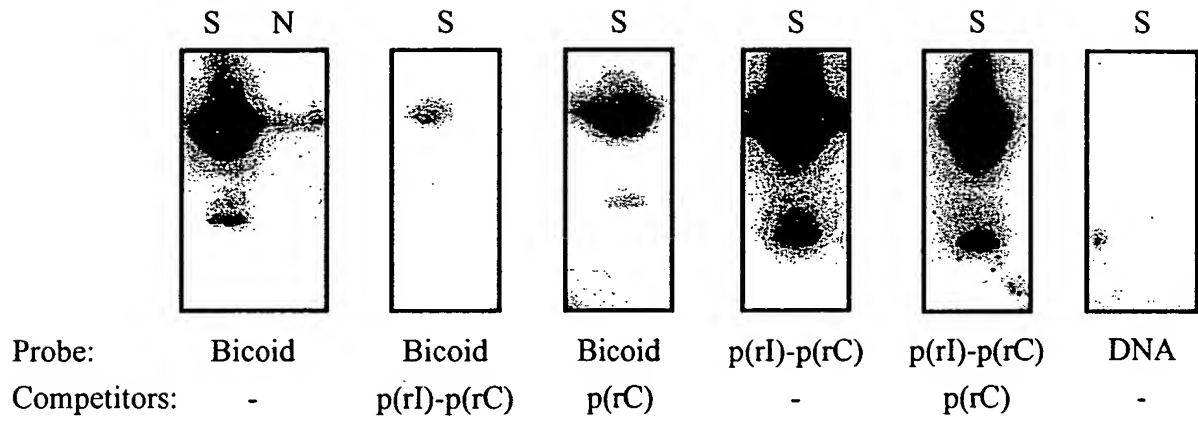


FIGURE 3

A



B

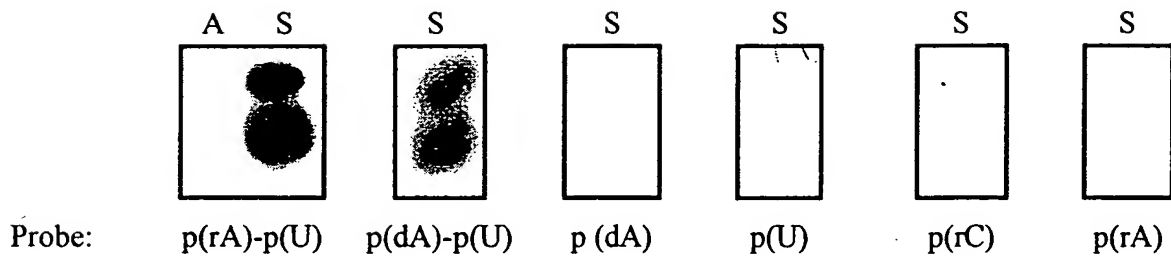


FIGURE 4

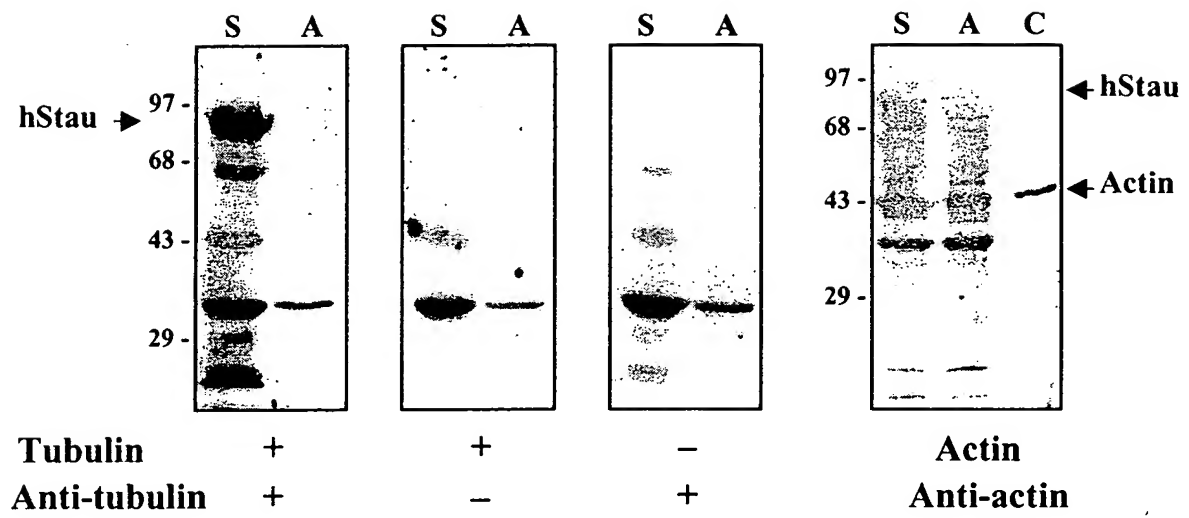
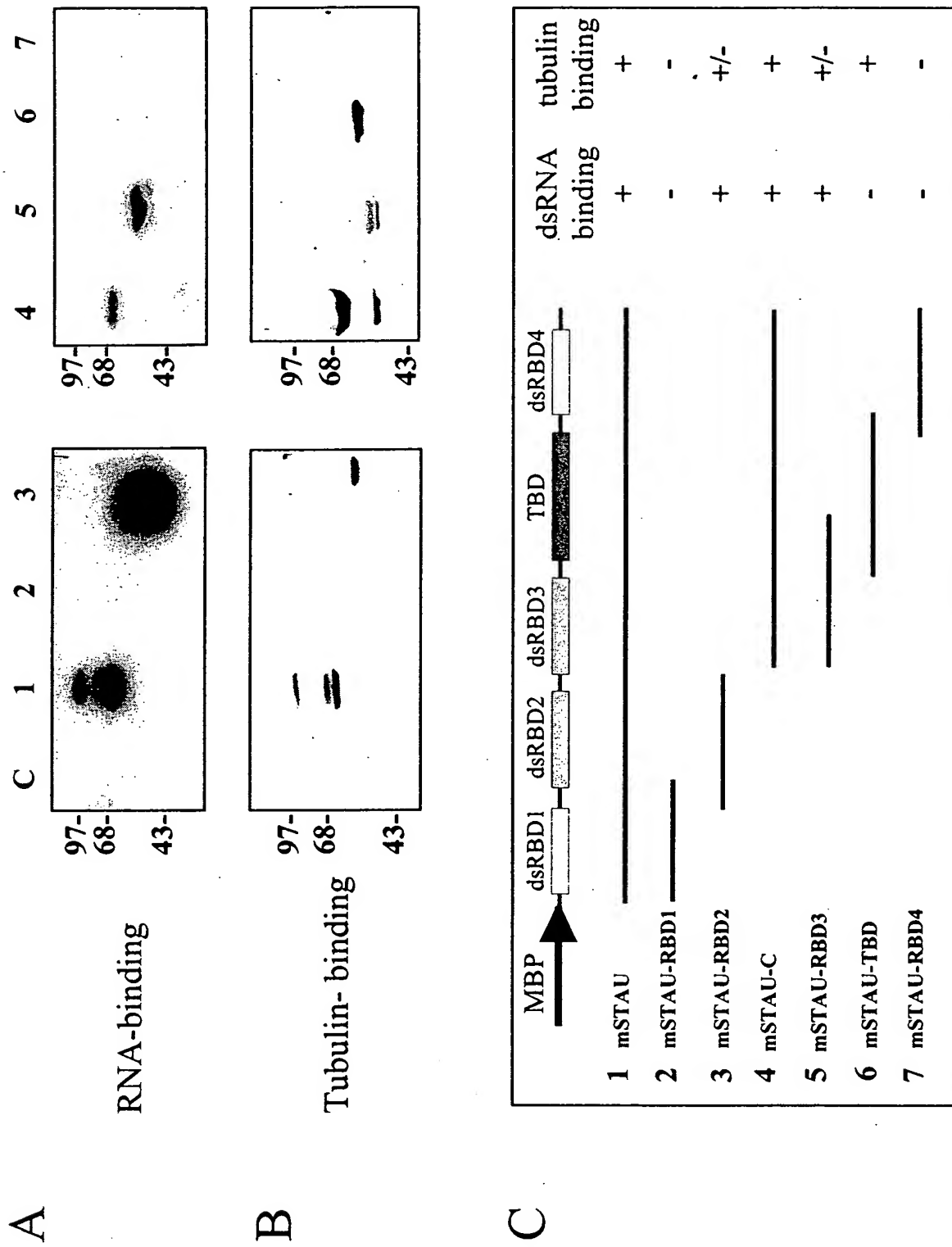


FIGURE 5



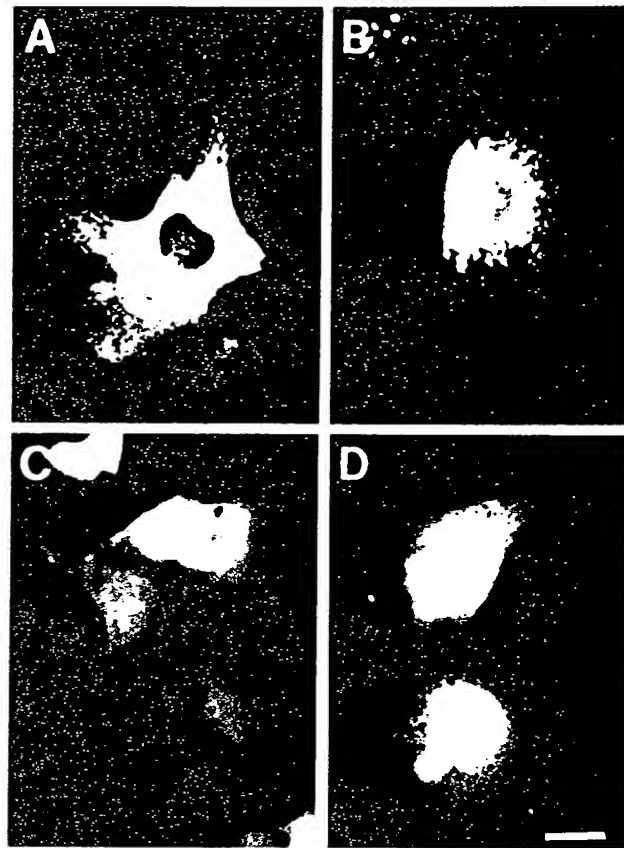


FIGURE 6

FIGURE 7

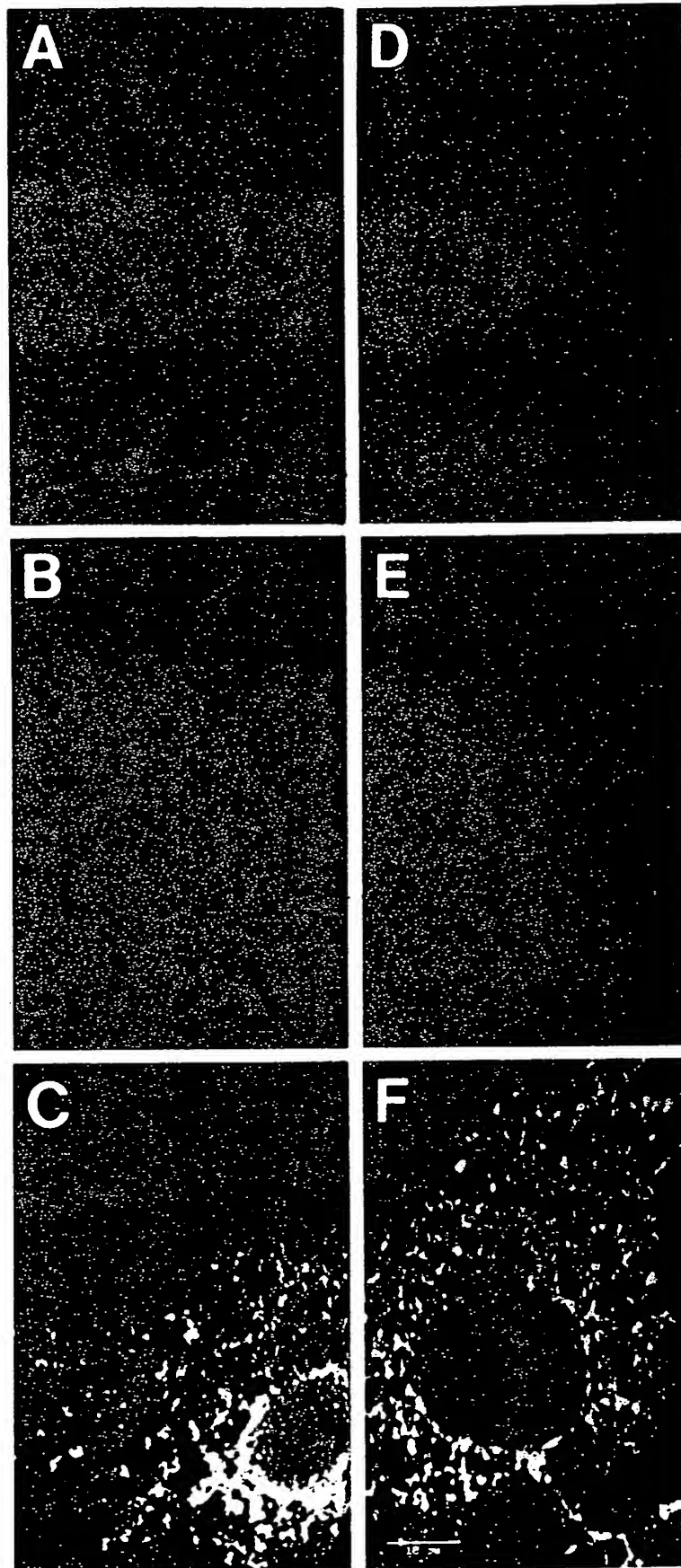
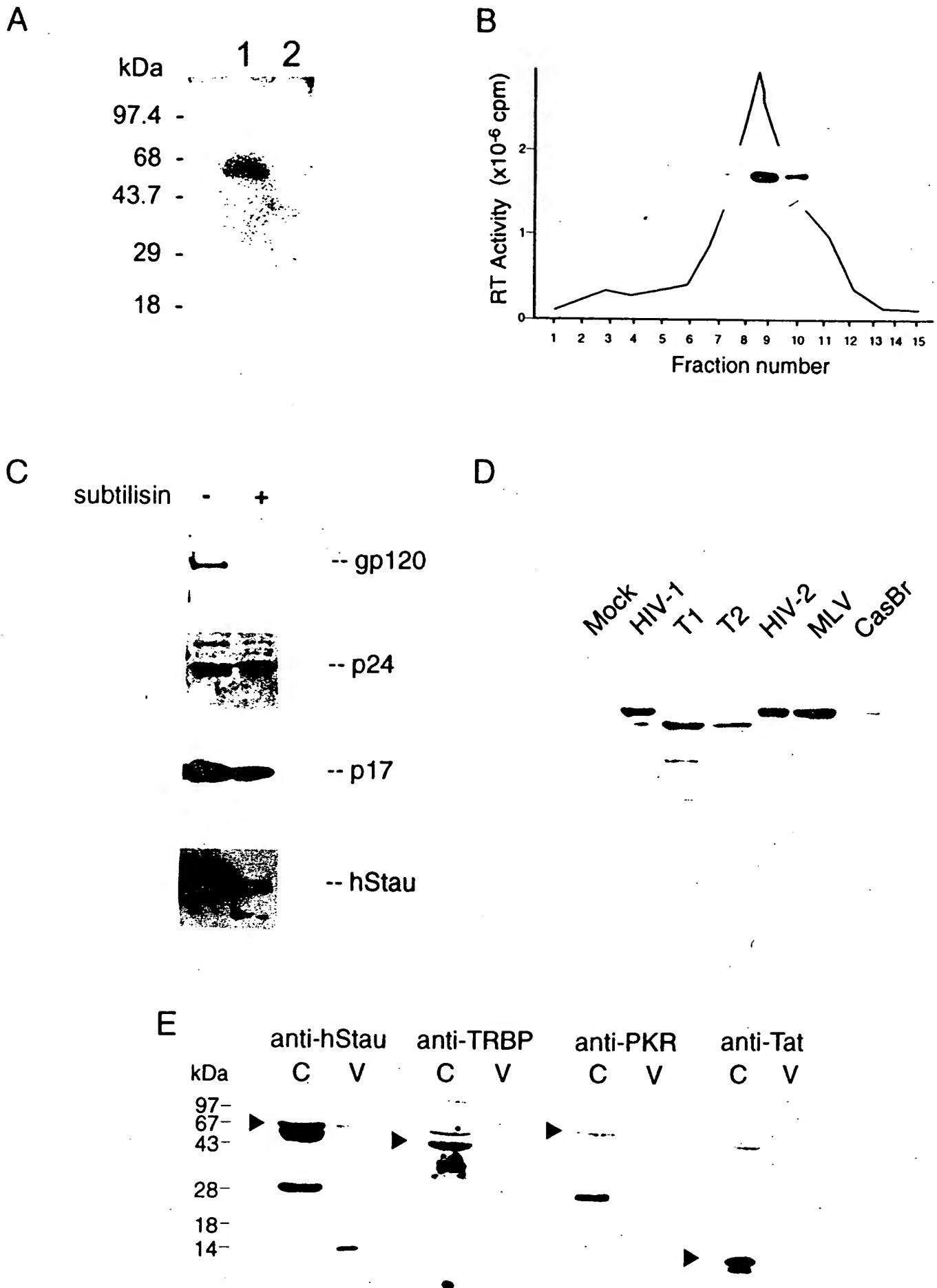


FIGURE 8



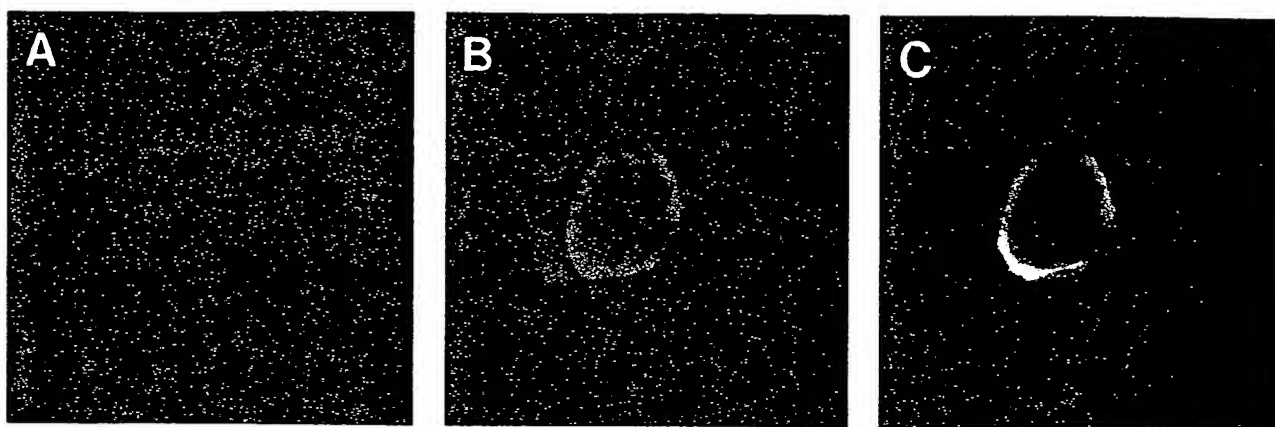


FIGURE 9

FIGURE 10

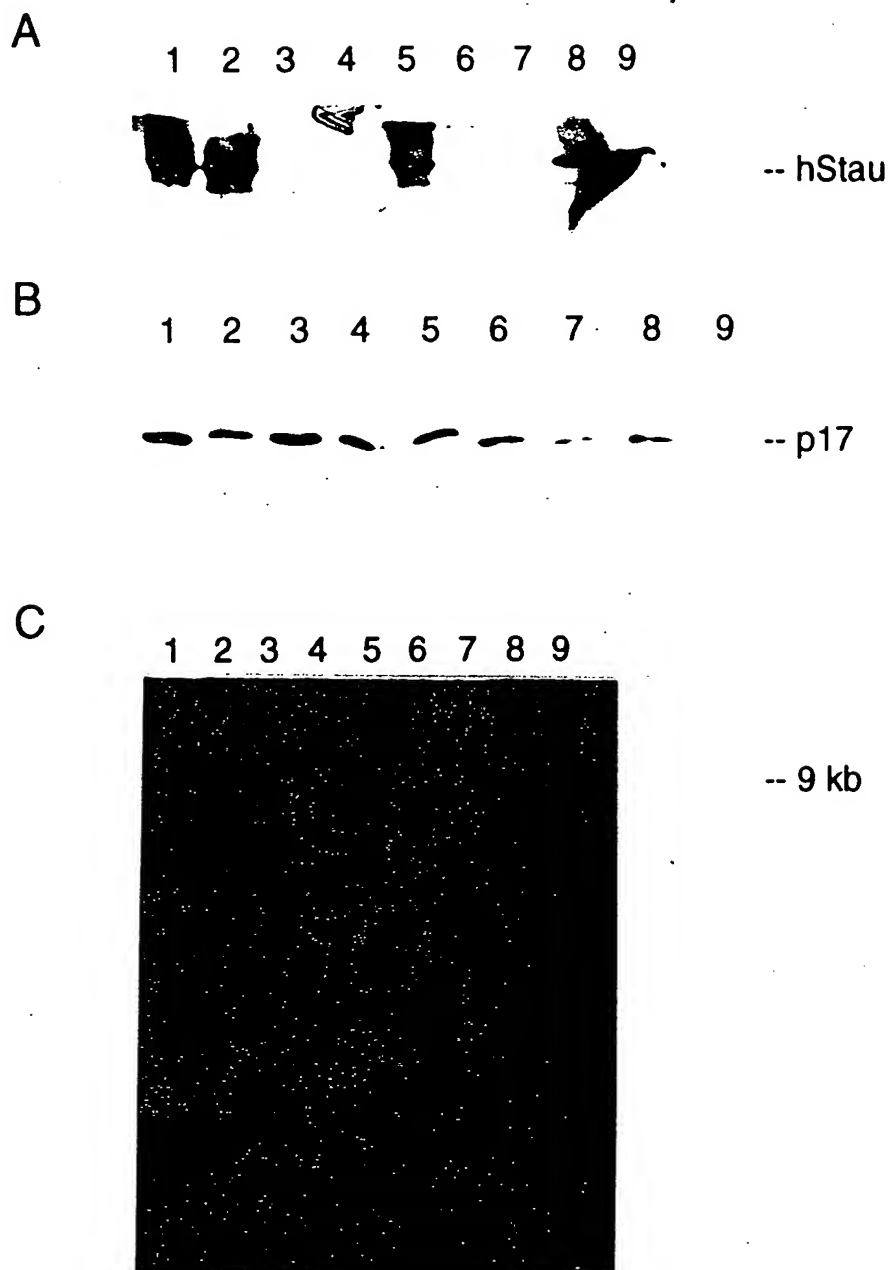
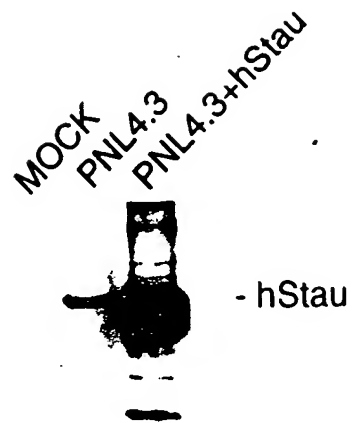
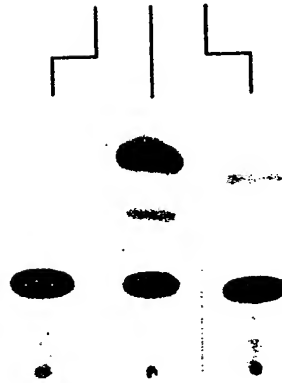


FIGURE 11

A



B



C

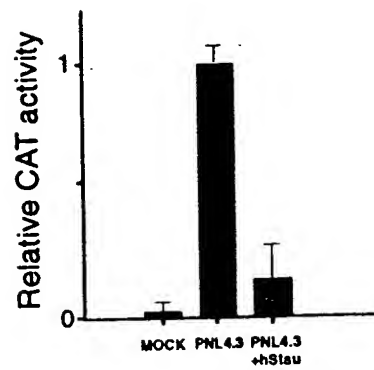


Figure 12

Primer combinations used in PCR amplifications for Gag constructs based on

HIV-1 HxB2 pr55^{Gag}

Gag mutants	Sense primer (5' → 3')	Antisense primer (5' → 3')
Pr55^{Gag}/Rluc	ACAGGTACCATGGGTGCGAGAGCGTCAG	ACAGGATCCCTTGTGACGAGGGGTCGTT
MA-CA/Rluc	ACAGGTACCATGGGTGCGAGAGCGTCAG	ACAGGATCCCCAAAACCTTGCCTTATG
CA/Rluc	ACAGGTACCATGCCTATAGTGCAGAACAT	ACAGGATCCCCAAAACCTTGCCTTATG
CA-p1/Rluc	ACAGGTACCATGCCTATAGTGCAGAACAT	ACAGGATCCCCAAATTCCTGGCCTTCC
CA-p6/Rluc	ACAGGTACCATGCCTATAGTGCAGAACAT	ACAGGATCCCTTGTGACGAGGGGTCGTT
MA/Rluc	ACAGGTACCATGGGTGCGAGAGCGTCAG	ACAGGATCCCGTAATTTGGCTGACCTG
p2-p1/Rluc	ACAGGTACCATGGCTGAAGCAATGAGCC	ACAGGATCCCCAAATTCCTGGCCTTCC
NC/Rluc	ACAGGTACCATGCAGAGAGGCAATTTTA	ACAGGATCCCATTAGCCTGTCTCTCAGT
p6/Rluc	ACAGGTACCATGCTTCAGAGCAGACCAG	ACAGGATCCCTTGTGACGAGGGGTCGTT

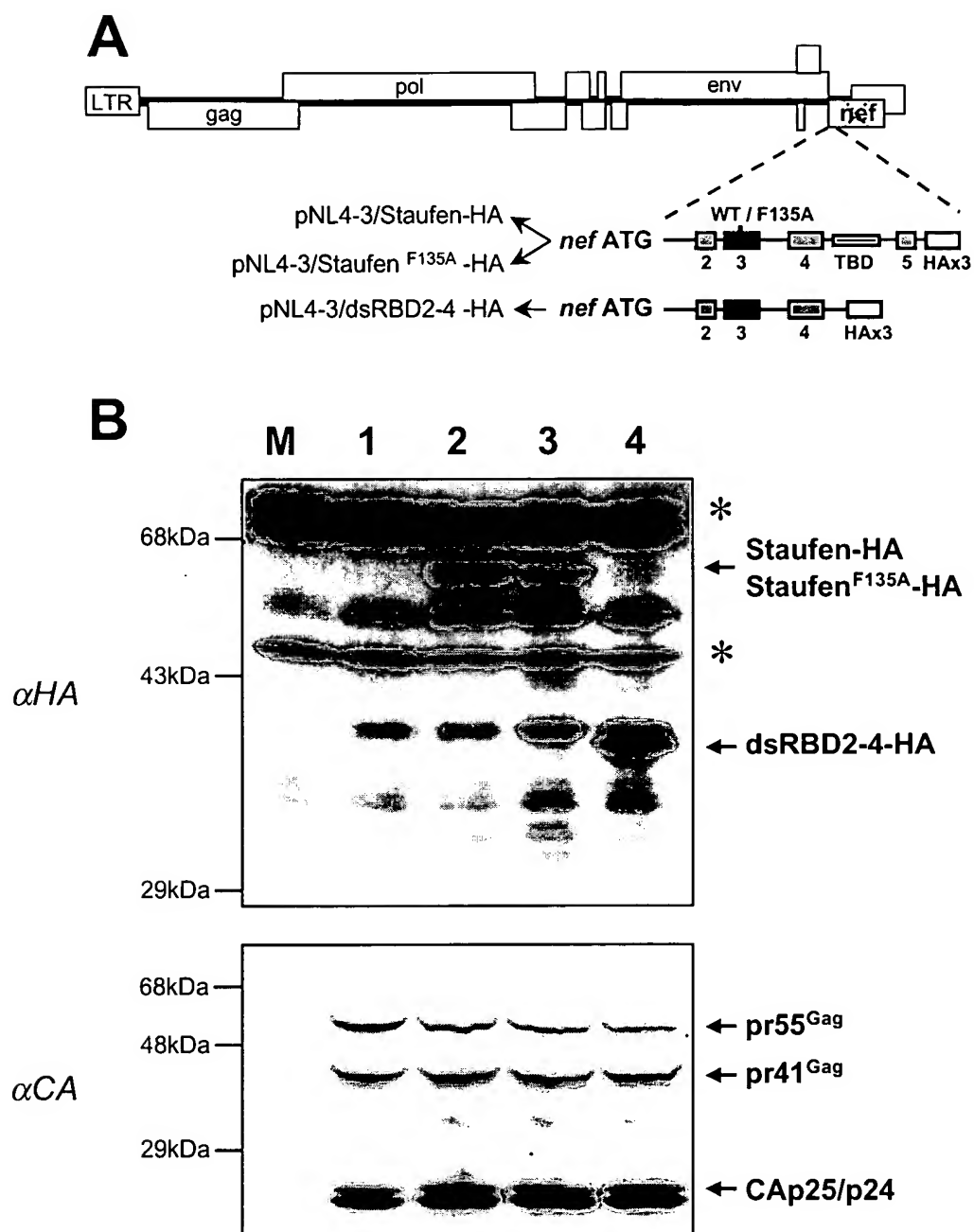


Figure 13

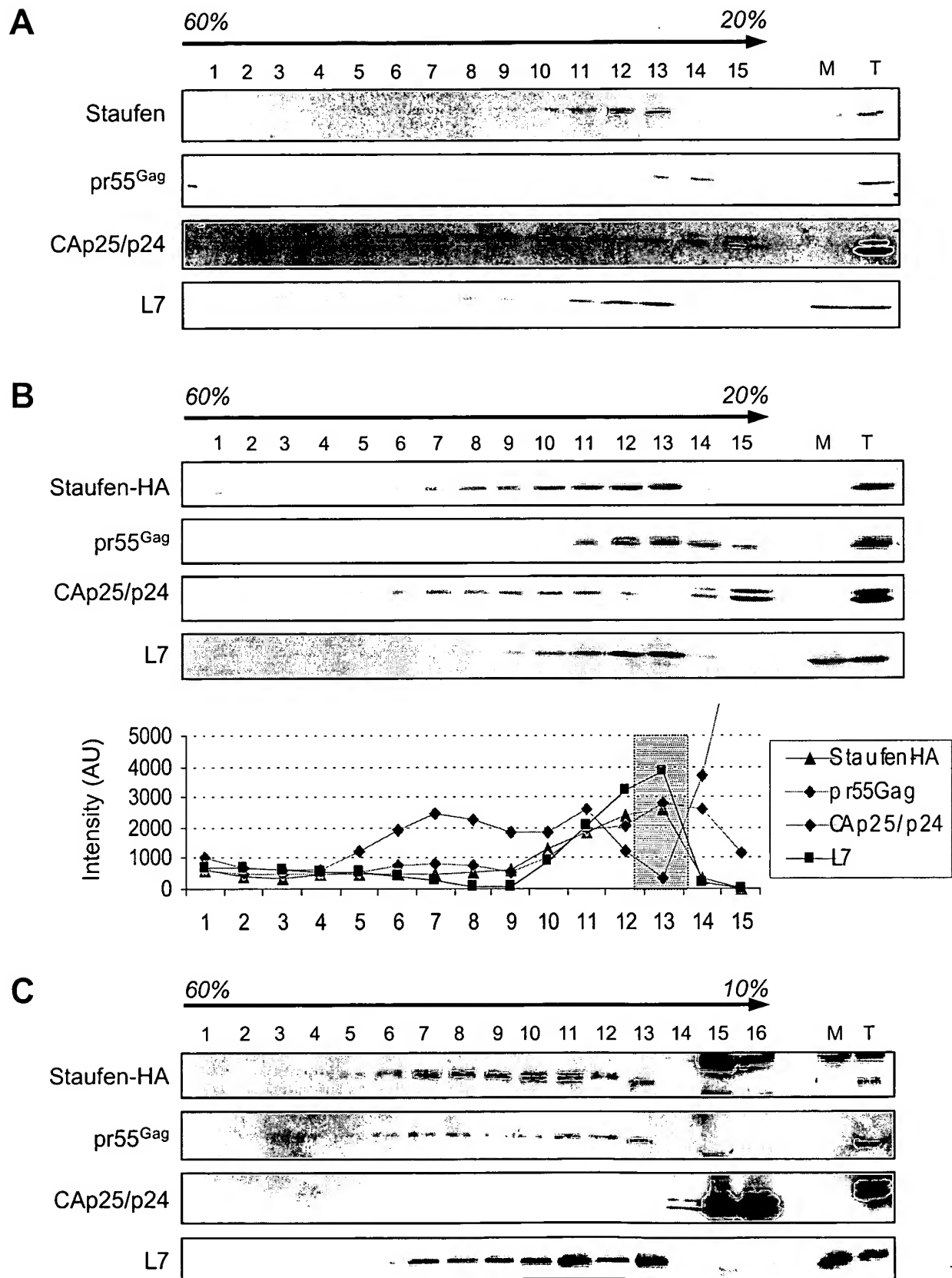


Figure 14

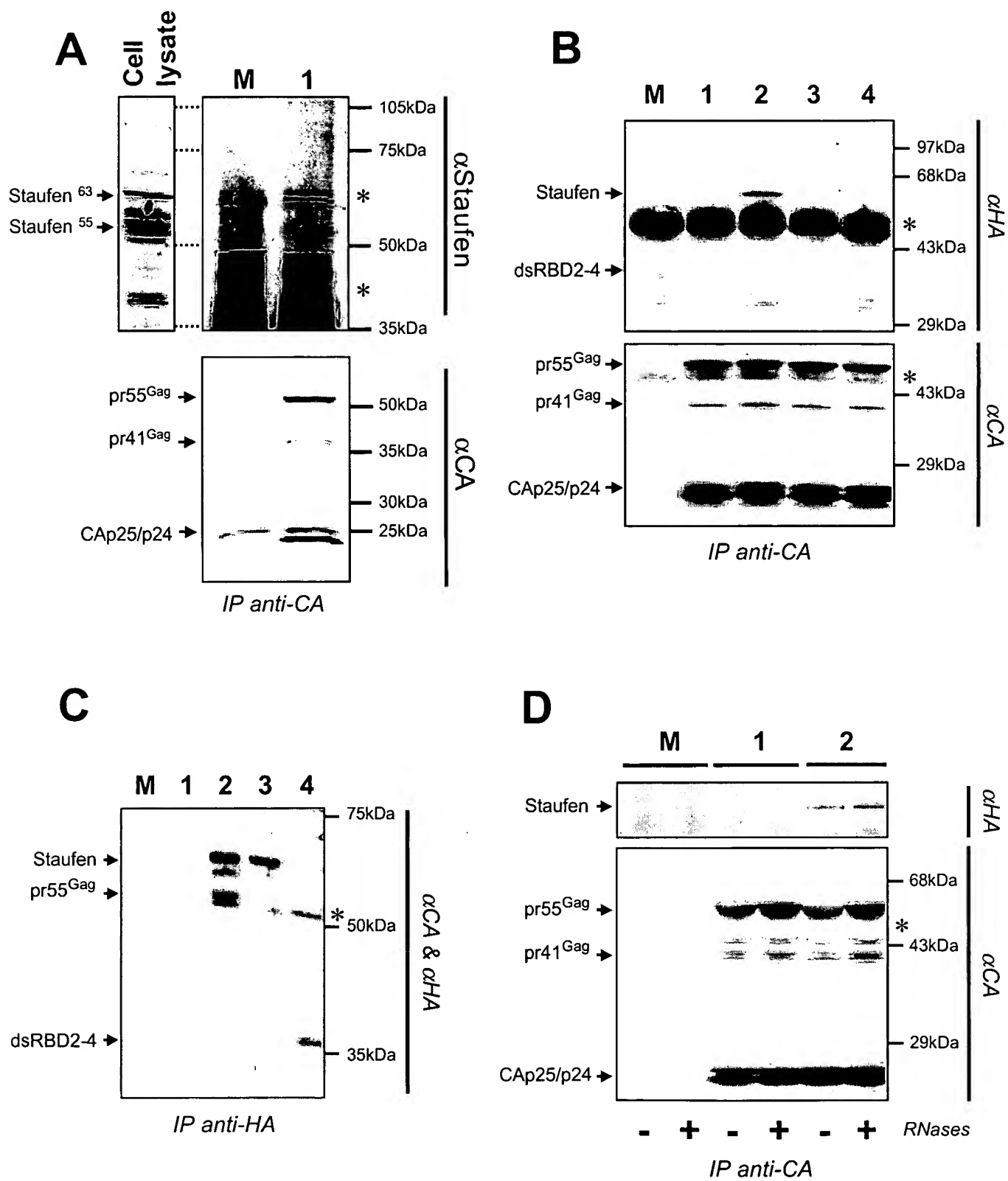


Figure 15

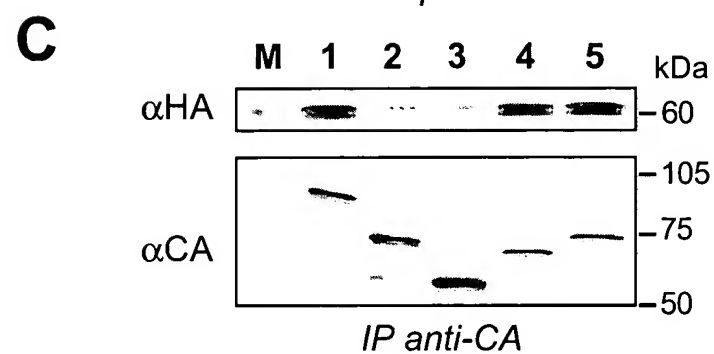
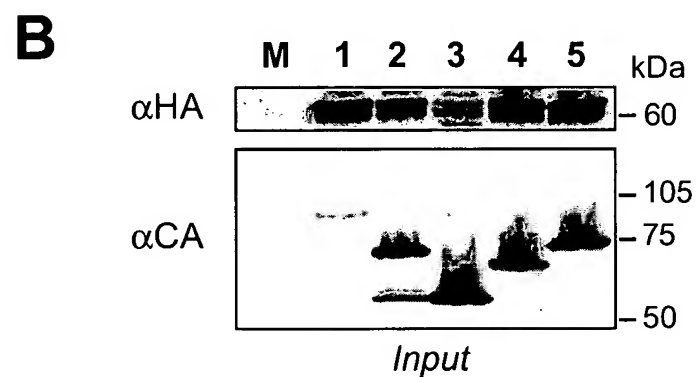
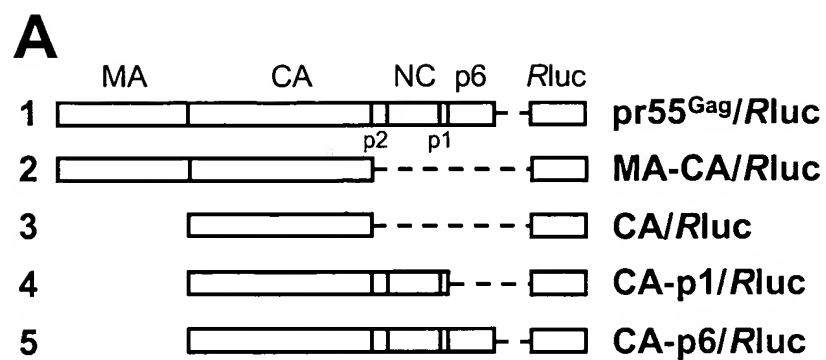


Figure 16

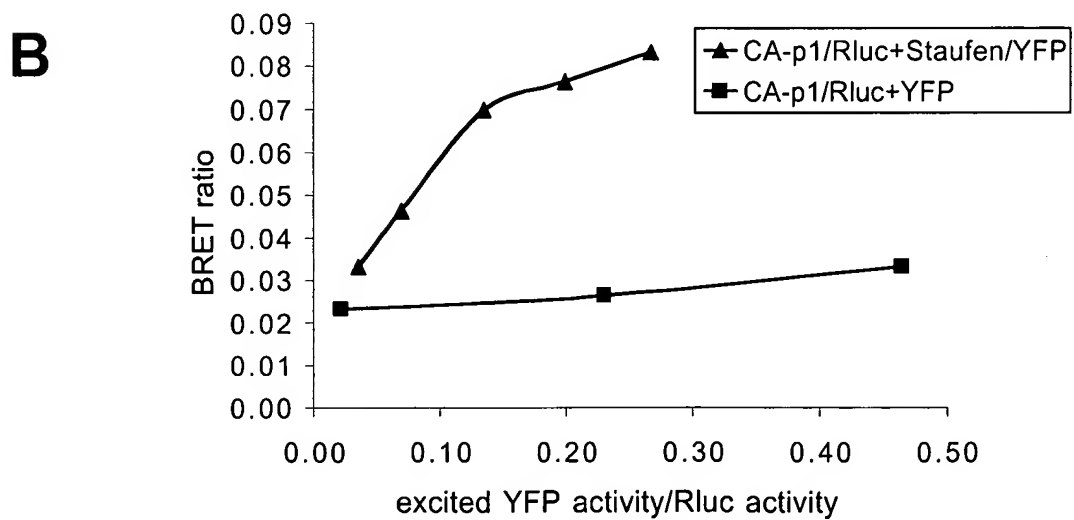
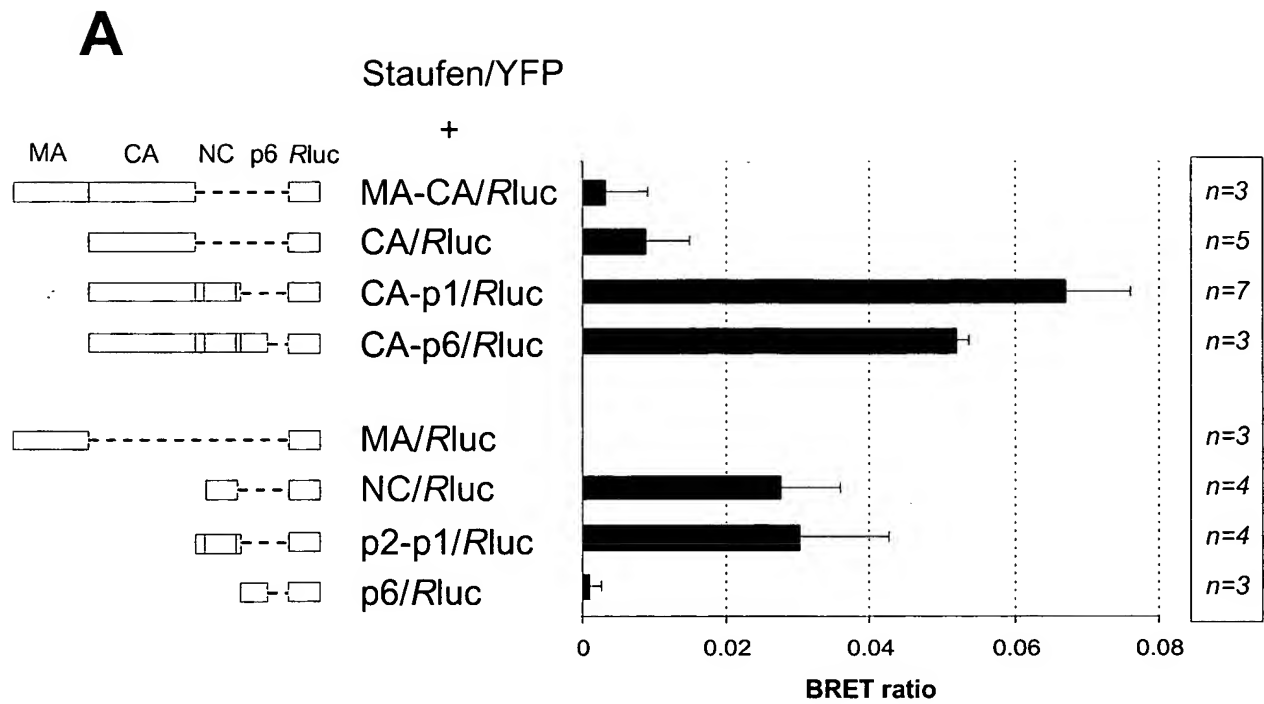


Figure 17

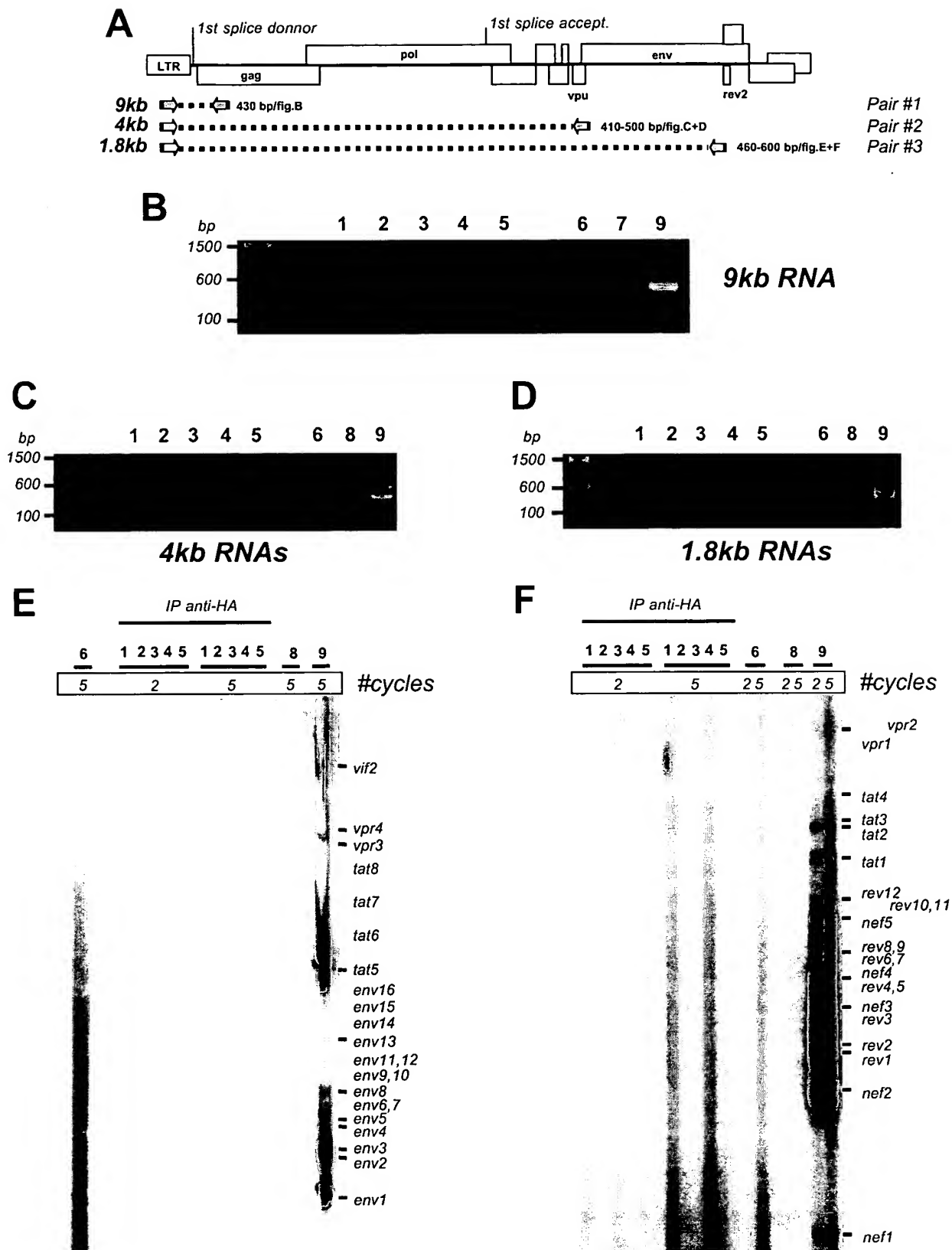


Figure 18

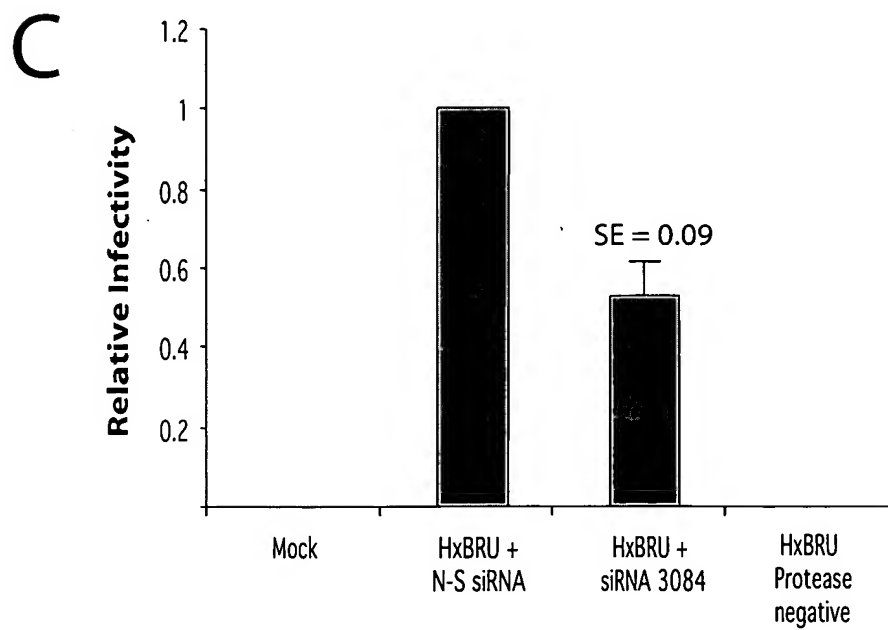
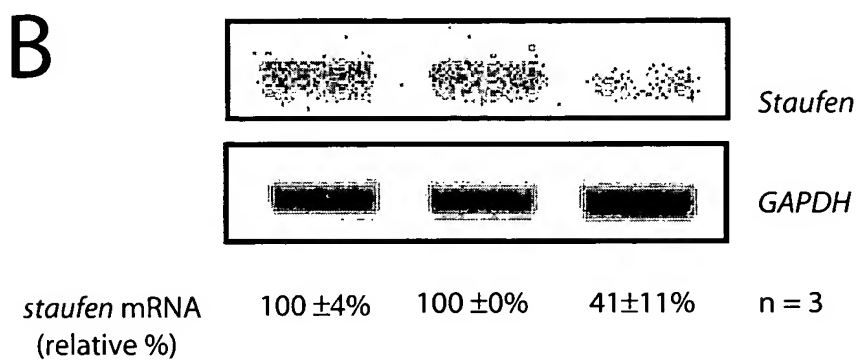
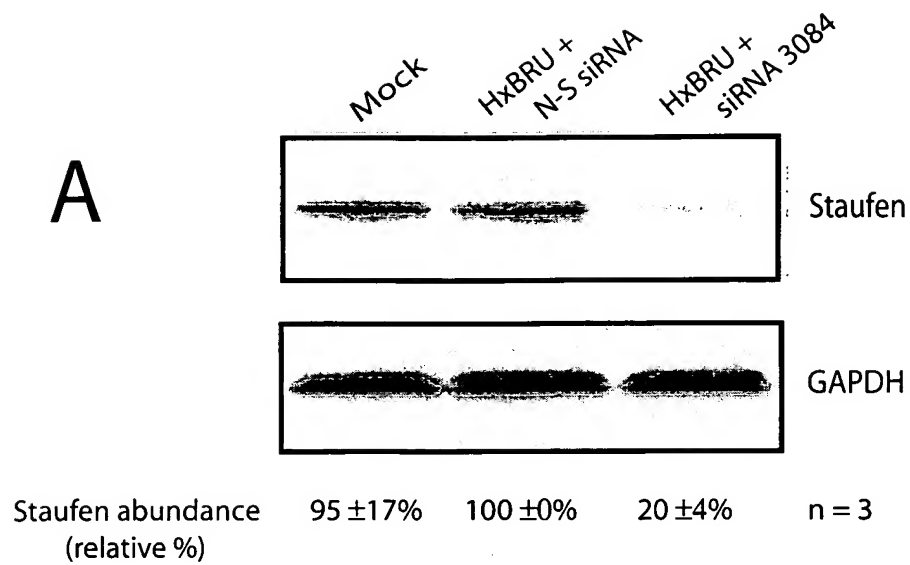


Figure 19

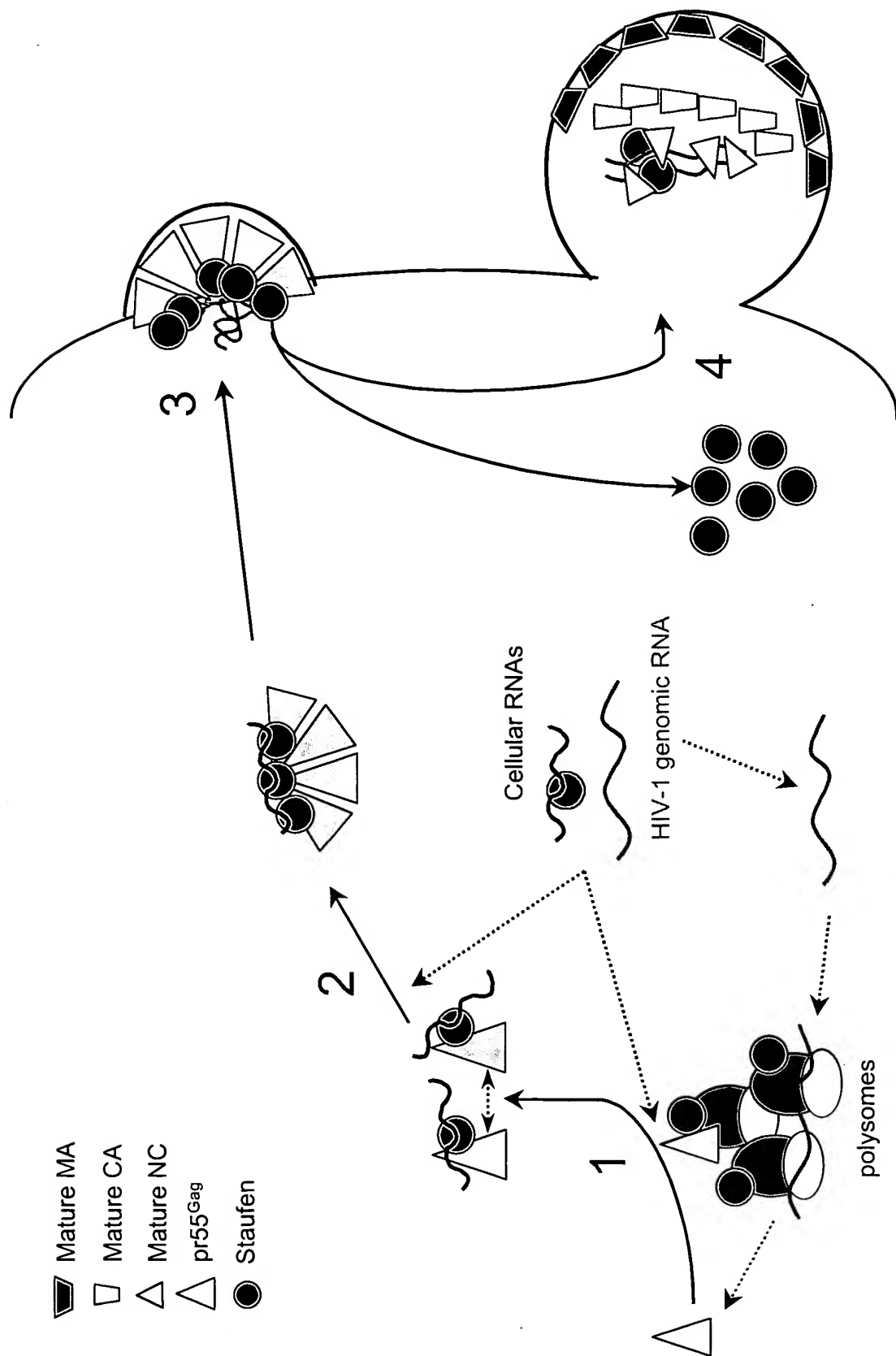


Figure 20

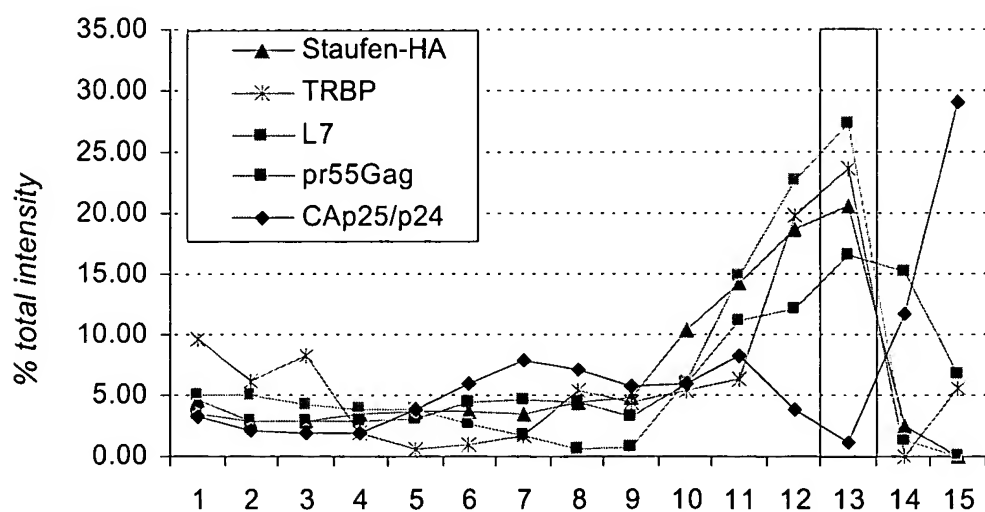
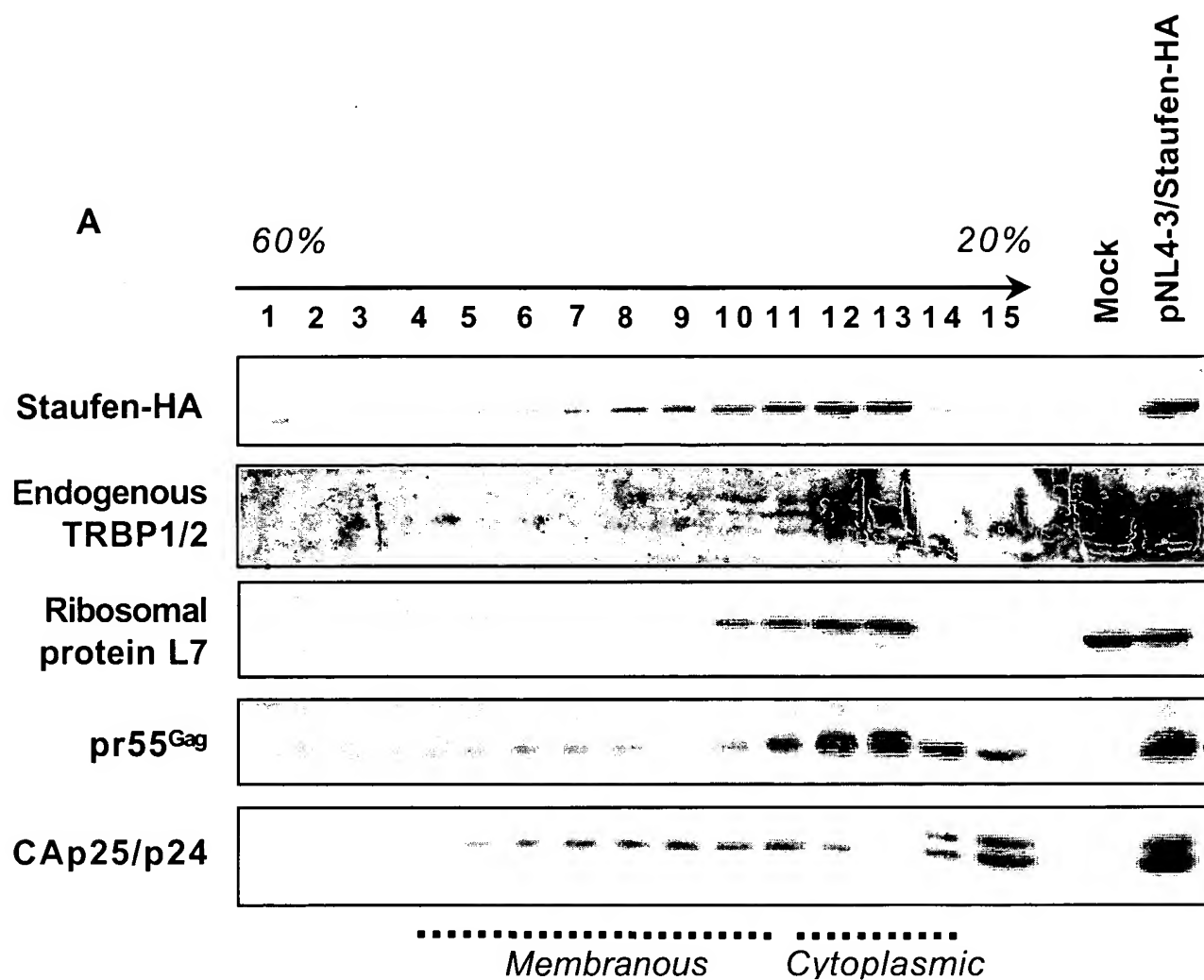


Figure 21A

B

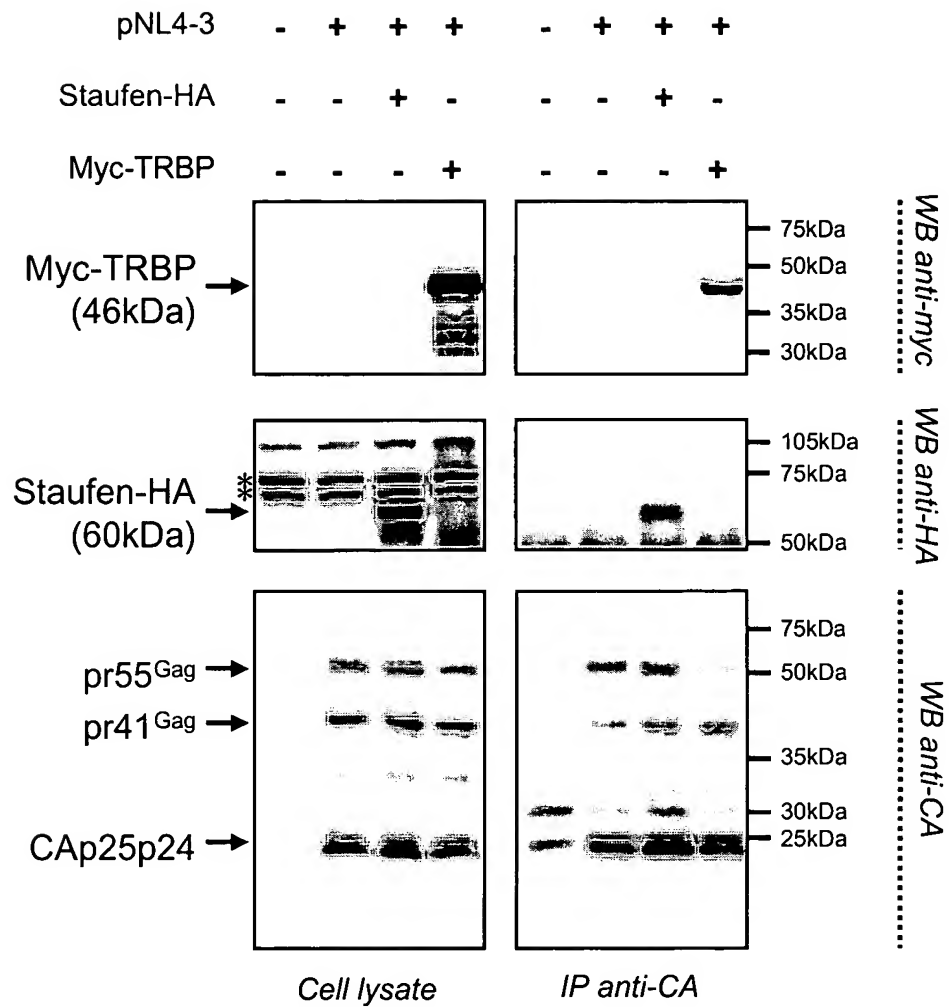


Figure 21B

Staufen is found in UHC-1 Promonocytic Cells

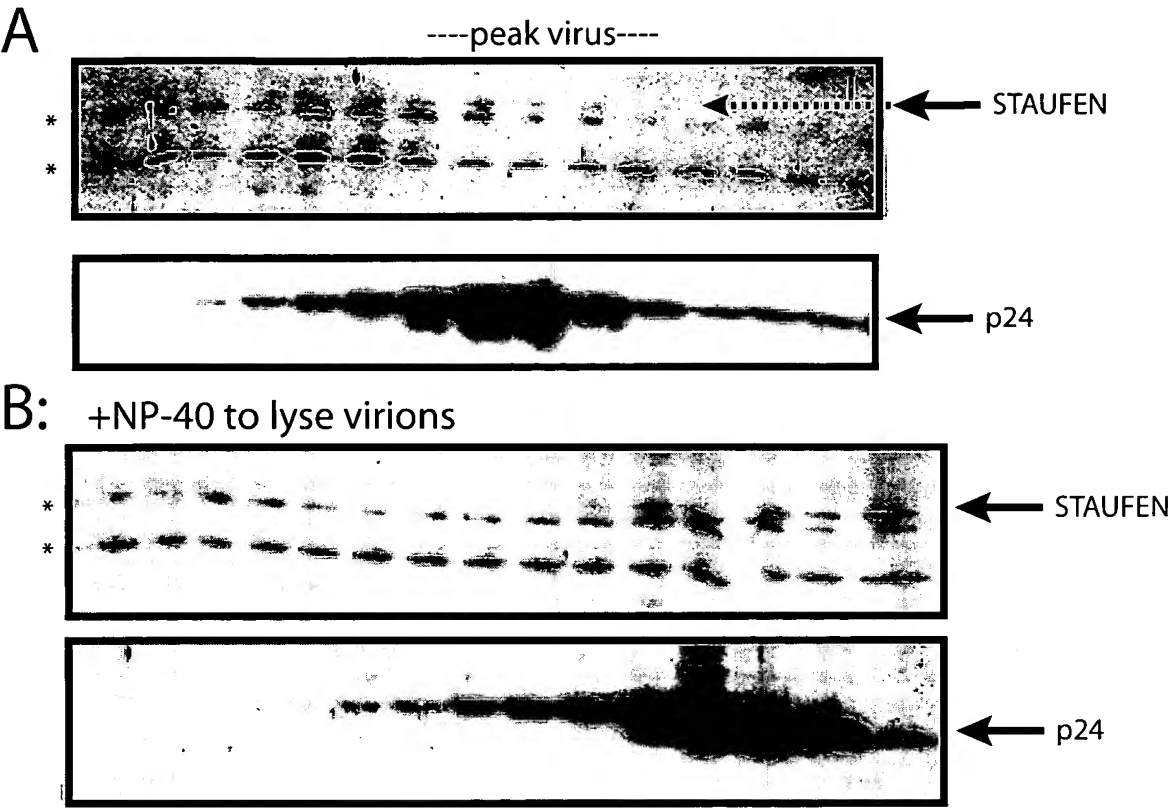


Figure 22

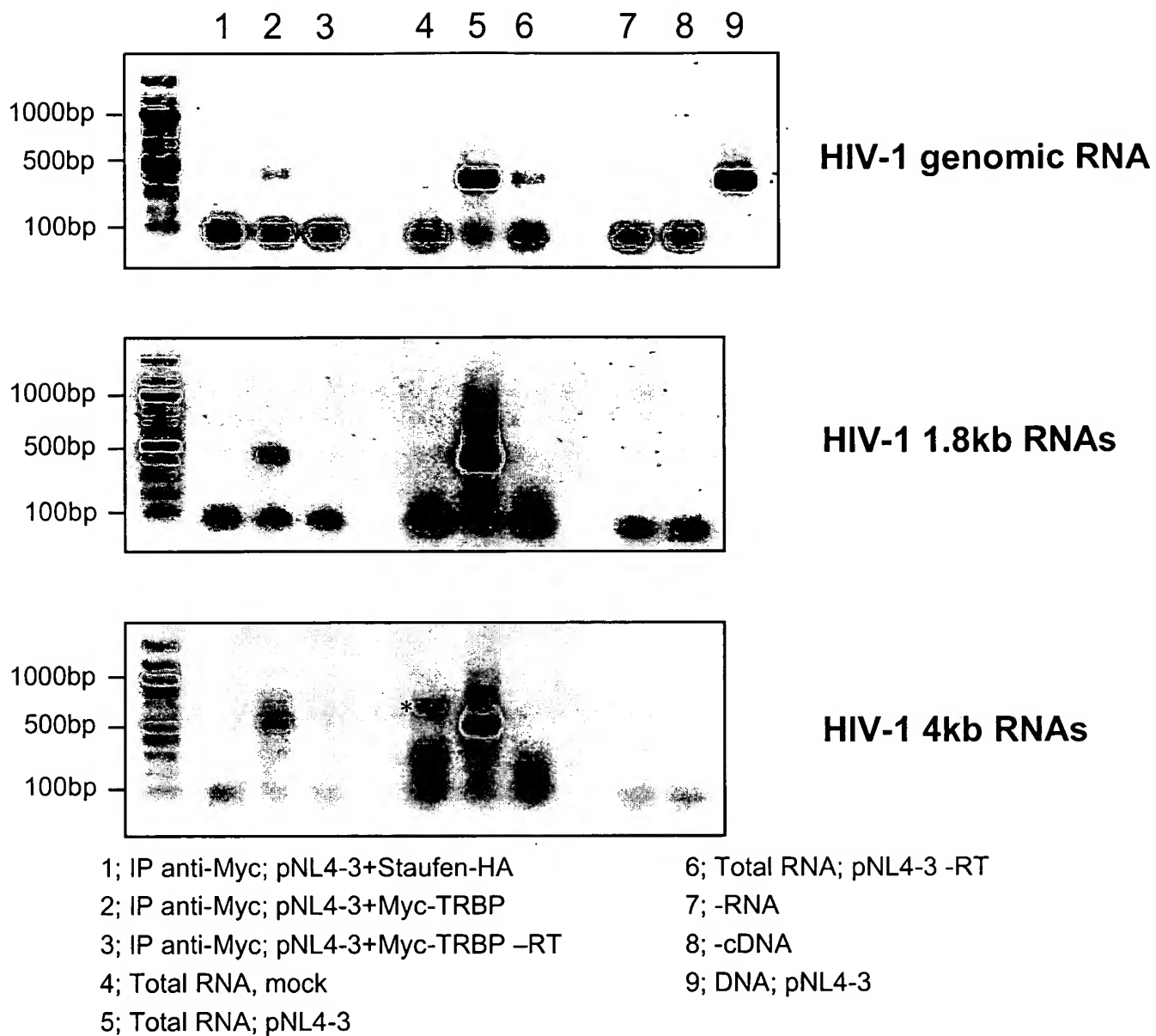


Figure 23